

GenCore version 4.5  
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OM nucleic - nucleic search, using sw model

Run on: August 27, 2001, 17:07:40 ; Search time 2462.53 Seconds  
(without alignments)  
2744.653 Million cell updates/sec

Title: US-09-784-340-3\_COPY\_197\_911  
Perfect score: 715  
Sequence: 1 atgaggtctgacaagtcagc.....gtttatagtaagcattag 715

Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 10228115 seqs, 4726426750 residues  
Total number of hits satisfying chosen parameters: 20456230

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

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257: gb\_est188:\*  
258: gb\_est189:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	409.6	57.3	671	175	BG249053	602361828
2	289.6	40.5	2099	192	AK008601	Mus muscu
3	280.8	39.3	906	21	A1529750	u182a02.y
4	245.4	34.3	889	150	BF533715	602073925
5	201.4	28.2	548	16	A1119588	u105c02.y
6	189.8	26.5	529	110	AW012524	u06a07.y
7	175.8	24.6	601	227	AQ371717	RPC111-15
8	162.6	22.7	777	16	A1116747	u28e05.y
9	158.2	22.1	2573	192	AK004971	Mus muscu
10	153.2	21.4	996	21	A1530408	u192f08.y
11	152.8	21.4	1896	192	AK002736	Mus muscu
12	152	21.3	923	21	A1529976	u187g04.y
13	151.4	21.2	697	153	BG427192	602494236
14	145.8	20.4	819	16	A1156939	u149c01.y
15	142	19.9	909	21	A1528459	u197f08.y
16	138.4	19.4	796	16	A1097842	u40e09.y
17	138.2	19.3	924	21	A1528431	u197d02.y
18	133	18.6	954	169	BF780608	602103156
19	133	18.6	1096	169	BF788115	602113339
20	132	18.5	881	2	AA109874	mm02f06.r
21	128.2	17.9	844	22	A1573962	u166f05.y
22	126.4	17.7	660	146	BF237356	602025029
23	126.2	17.7	595	155	BG562901	602581752
24	125.6	17.6	685	18	A1324412	mm02f06.y
25	123.6	17.3	1059	169	BF784658	602110381
26	123.4	17.3	707	14	AA986985	uc80n04.y
27	119	16.6	785	153	BG429706	602493711
28	119	16.6	787	153	BG430305	602502309
29	117	16.4	688	169	BF782813	602107673
30	116	16.2	756	153	BG429801	602494817
31	114.6	16.0	855	169	BF784106	602110061
32	114.6	16.0	954	169	BF787491	602113909
33	114.2	16.0	821	153	BG402643	602465575
34	111.6	15.6	932	148	BF383536	602044428
35	110.4	15.4	901	153	BG400539	602464778
36	109.6	15.3	803	169	BF788917	602104648
37	109	15.2	754	19	A1386294	mm75f08.y
38	106.4	14.9	589	16	A1119259	u24d05.y
39	104.2	14.6	665	146	BF236531	602028707
40	103.6	14.5	741	146	BF235182	602026457
41	103	14.4	728	153	BG433410	602501120
42	101.8	14.2	884	150	BF533130	602073667
43	101.8	14.2	905	150	BF532101	602073223
44	101.6	14.2	527	17	A1225575	u105f12.y
45	100.4	14.0	457	153	BG412991	ia83d08.y

## ALIGNMENTS

RESULT 1  
 BG249053  
 LOCUS 602361828F1 NIH\_MGC\_89 Homo sapiens cDNA clone IMAGE:4470199 5',  
 DEFINITION mRNA sequence. EST 13-FEB-2001  
 ACCESSION BG249053  
 VERSION BG249053.1  
 KEYWORDS EST. GI:12758869  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 REFERENCE 1 (bases 1 to 671)  
 AUTHORS NIH-MGC http://mgc.nci.nih.gov/  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.

Email: cgapbs-re@mail.nih.gov  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Life Technologies, Inc.  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.lnl.gov  
 Plate: LLM10287 row: h column: 08  
 High quality sequence stop: 661.

## FEATURES

Location/Qualifiers  
 1..671  
 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:4470199"  
 /clone\_lib="NIH\_MGC\_89"  
 /tissue\_type="hypertrophied, cell line"  
 /lab\_host="PH10B (phage-resistant)"  
 /note="Organ: kidney; Vector: pCMV-SPORT6; Site: 1: NotI; Site: 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.3 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH\_MGC Library."  
 BASE COUNT 206 a 123 c 153 g 189 t  
 ORIGIN

Query Match 57.3%; Score 409.6; DB 175; Length 671;  
 Best Local Similarity 95.3%; Pred. No. 3.1e-104;  
 Matches 509; Conservative 0; Mismatches 14; Indels 11; Gaps 8;

QY 167 tgactcaactcaagccttcgttaattgactacaggaagccttcgtgactgaattgag 226  
 Db 11 TGACTCACTCAAGCCCTTGGTTAA-TGACTACAGGAGCTTCTGCTGAA--TTGAGG 67  
 QY 227 tggctcatatgccagagcagacagagagagagagagagagagagagagagag 286  
 Db 68 TGTCTCATATGCCAGGAGCAGACAGAGAGAGAGAGAGAGAGAGAGAGAGAG 126  
 QY 287 atgtcttgcagcgttatcaactcagcgtgcaatcagttataattataatgattttttgtg 346  
 Db 127 ATGCTCTGCCAGGCTTATCAACCTGGCAATCAGTTATAA--TTAATGATTTTGTGTTG 186  
 QY 347 aaataagaggaactttaaaatgatgtgagagacttaatacaatcagacactatga 406  
 Db 187 AAATAAGAGGAAGCTTTAAATATGATGTGAGAGCTTTATTTACAAATCAGACGCTTATGA 246  
 QY 407 agaagctacagaaacaaactacgactgaacgcttaagacccgtgattcccggtgag 466  
 Db 247 AGAAGCTACAGGAACCAACTACGATGATGATGATGATGATGATGATGATGATGATGATGATG 306  
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 Db 307 ACCTGATGCTGAGTGTCTTGTGAGTCCCTTTGTGCTCACTAGATTTCTGTTAGGA 366  
 QY 526 ggcaatattggagcgaagct-gtgggaactccagctccn-cttctctatgtacctgtgc 583  
 Db 367 GGCAATATGGAGGAAGCTGGTGGGAAACTTCCAGCTCCAGCTTCTCTATGTACCTGTGC 426  
 QY 584 ctatgacaggaactaaacagacagaa-tgacctttctggaagagat---aaaaattcaatg 639  
 Db 427 CTATGACAGGACTAACAGACAGAGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 486  
 QY 640 ctttcagtttcttcactctctgattcaggattacagactcatttttgggaa 693  
 Db 487 CTTTCAGTCTTTGTGCCACTCTCTGGATTACGATTACGATTACGATTACGATTACGATTACGATT 540

RESULT 2  
 AK008601  
 LOCUS AK008601 2099 bp mRNA HTC 08-FEB-2001  
 DEFINITION Mus musculus adult male small intestine cDNA, RIKEN full-length enriched library, clone:2010321J07, full insert sequence.

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VERSION	AK008601.1	/protein_id="BAB25770.1"				
KEYWORDS	CAP trapper.	/db_xref="GI:12842885"				
SOURCE	Mus musculus (strain:C57BL/6J) adult male small intestine cDNA to mRNA, clone.lib:RIKEN full-length enriched mouse cDNA library clone:2010321J07.	/translation="MVSEKCVAAFFLLQLWAGCGFCVLYWPCDMSHNLKLTILE ELGARGHEVTVLKYPSTIIIDQSCIRSLPH'ENIPILYETAEENRLEINIANLVNIVELV LSLAEAKTLODFLOVTFQDFESICRSLV'NQKFMKLDRAQYDVIIVPVPVCGELV AEVLQIPRVYTLRFSGMVG'YMEKHGCGQLPTPLSGVYVVMVSELNTMTTERVKNMFSL LFEVWLQYDFAPWQDYSETLGRFTTH'KTVGEADLWLR'YVWDVFFPRPLPNFFEF VGGHCRKAPKLPKREMBEFVOSSEHGYYV'FSLGSMVKNLTERKANLIASVLAQIPQK VLMRYSGKKPAILAHNTRFLFNWIPONDLLGHPTKAFITHGCTNGIYELVHGYPMVG VMLGDDPHNIAHMEAKGAAKVISISTN'DLLLSAVRAVINEFSYENAMRLSRIHH DQPKVFLDRVFEVIEFVNRHGAKHLRVAADHLSWFOYHSLDVIFGLLLCVVTLTFII TKFCFLVCQCKLYMKESKKMGRKKKN"				
ORGANISM	Mus musculus					
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.					
AUTHORS	Carninci,P. and Hayashizaki,Y.					
JOURNAL	High-efficiency full-length cDNA cloning					
REFERENCE	Methods Enzymol. 303, 19-44 (1999)					
TITLE	2 (sites)					
JOURNAL	Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Konno,H., Akiyama,J., Nishi,K., Kitsuunai,T., Tashiro,H., Itoh,M., Kikuchi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwaki,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsura,S., Okazaki,Y., Muramatsu,M., Inoue,Y. and Hayashizaki,Y.					
MEDLINE	RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer					
AUTHORS	Genome Res. 10 (11), 1757-1771 (2000)					
TITLE	20530913					
JOURNAL	4 (sites)					
MEDLINE	The RIKEN Genome Exploration Research Group Phase II Team and PANTOM Consortium.					
AUTHORS	Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)					
TITLE	5 (bases 1 to 2099)					
JOURNAL	Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Aono,H., Arai,A., Arakawa,T., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Harada,A., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Imofani,K., Ishii,Y., Itoh,M., Izawa,M., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,K., Nishi,K., Nomura,K., Nomura,K., Sakai,C., Sakai,K., Sano,H., Okido,T., Owa,C., Saito,H., Saito,R., Shingawa,A., Shiraki,T., Sasaki,D., Shibata,K., Shibata,Y., Shingawa,A., Takahashi,F., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,A., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.					
REFERENCE	Direct Submission					
AUTHORS	Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gs.riken.go.jp, URL:http://genome.gsc.riken.go.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)					
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FEATURES  
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Qy 241 caggacagacagagaagaataat-----ttgtgacctagctctgaatgctc 291  
 Db 269 TATGAAATCGAGACACGTCGAGAAATCGTTTAAATGAGATTGCAAAATCTAGCTGTGAATGTC 328  
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 LOCUS uo06a07.y1 Sugano mouse liver mlia Mus musculus cDNA clone  
 DEFINITION IMAGE:2582580 5' similar to SW:UDBG.RABIT.019103  
 UPD-GLUCURONOSYLTRANSFERASE 2B16 PRECURSOR, MICROSOMAL ;, mRNA  
 sequence.  
 ACCESSION AW012524  
 VERSION AW012524.1 GI:5861302  
 KEYWORDS EST.  
 SOURCE house mouse.  
 ORGANISM Mus musculus  
 Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 1 (bases 1 to 529)  
 AUTHORS Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,  
 Underwood,K., Stepien,M., Theising,B., Allen,M., Bowers,Y., Person  
 ,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurk,R., Ritter  
 ,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,  
 Waterston,R. and Wilson,R.  
 TITLE The WashU-NCI Mouse EST Project 1999  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Marra M/WashU-NCI Mouse EST Project 1999  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810  
 Email: mouseest@watson.wustl.edu  
 This clone is available royalty-free through LLNL ; contact the  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 MGI:1022168  
 Seq primer: custom primer used  
 High quality sequence stop: 492.

FEATURES  
source

1. 529  
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 /strain="C57BL"  
 /db\_xref="taxon:10090"  
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 /clone\_lib="Sugano mouse liver mlia"  
 /sex="female"  
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 /note="Organ: liver; Vector: pME18S-FL3; Site\_1: DraIII  
 (CACTGTG); Site\_2: DraIII (CAACATGTG); 1st strand cDNA  
 was primed with an oligo(dt) primer  
 [ATCGGCCCTTTTTTTTTTTTTTTT]; double-stranded cDNA was  
 ligated to a DraIII adaptor [TGTGGCCTACTGG], digested  
 and cloned into distinct DraIII sites of the pME18S-FL3  
 vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should  
 be used to isolate the cDNA insert. Size selection was

performed to exclude fragments <1.5kb. Library  
 constructed by Dr. Sumio Sugano (University of Tokyo  
 Institute of Medical Science; Custom primers for  
 sequencing: 5' end primer CT: TGCTTAAAAAGCTGCG and 3' end  
 primer CGACCTGCAGCTCGACACA.  
 BASE COUNT 147 a 101 c 131 g 150 t  
 ORIGIN

Query Match 26.5%; Score 189.8; DB 110; Length 529;  
 Best Local Similarity 64.3%; Pred. No. 1.5e-2;  
 Matches 322; Conservative 0; Mismatches 7; Indels 12; Gaps 2;  
 Qy 1 atgaggctcagcaagtcagcttttggtatttctgctcgtcagctctctctgtgtgtgtgt 60  
 Db 32 ATGGCTCTCTAAAAAATGTTGGCTCATTTTCTGTCTGAGCTTGTCTGGCGGGGTGT 91  
 Qy 61 ggattctgtggaaagtcctgggtgctcctgtgacatgajccatttggttaattgtcaag 120  
 Db 92 GGATTCTGCAGCAAGGTCCTCGTGTGGCCCTGTGATATGAACACTGGCTGAATCTAAAG 151  
 Qy 121 gtcatctagaagagctcatagtgagggccatgaggtaaagtattgactcactcaag 180  
 Db 152 ACTATTCTTGGAGGCTTGGGCAAGAGGGCAGAGTAACAGTCTCTGAAATACCCCA-- 209  
 Qy 181 ccttcgttaattgactacaggaagcctctgcattgaaatttgaggtggttccatgccca 240  
 Db 210 -GTATCATCATATCATGAGCTAAACGTATTCCACTGCTGAGATATATTCCTTTCTG 268  
 Qy 241 caggacagacagagaagaataatgaaatat-----ttgtgacctagctctgaatgctc 291  
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 Db 329 ATTCCAAACCTGTCTACTGTGGGAGCAGCAAAAACATTACAGACTCTTCTTCACAGTA 388  
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 Db 449 CTACGGNATGCACAAATATGATGTAGTGTATAGACCCCTGCTGCTCCCTGTGGAGAGTTG 508  
 Qy 472 atggctgagttgctccagctc 492  
 Db 509 GTGGCAGAGTGCTTCAGATC 529

## RESULT 7

AW0371717/c 601 bp DNA GSS 20-MAY-1999  
 LOCUS RPC111-155J15.TV RPCI-11 Homo sapiens genomic clone RPCI-11-155J15,  
 DEFINITION DNA sequence.  
 ACCESSION AW0371717  
 VERSION AW0371717.1 GI:4342740  
 KEYWORDS GSS.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.  
 1 (bases 1 to 601)  
 REFERENCE Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and Venter  
 ,J.C.  
 TITLE Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready  
 Map Building  
 JOURNAL Unpublished (1997)  
 COMMENT Other-GSSs: RPC111-155J15.TJ  
 Contact: Shaying Zhao, William Nierman, Mark Adams  
 Department of Eukaryotic Genomics  
 The Institute for Genomic Research  
 9712 Medical Center Dr., Rockville, MD 20850

MGI:930052  
 IMAGE Consortium (info@image.llnl.gov) for further information.  
 Seq primer: custom primer used  
 High quality sequence stop: 458.  
 Location/Qualifiers  
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         /organism="Mus musculus"  
         /strain="C57BL"  
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/sex="female"
/dev_stage="adult"
/lab_host="DH108"
/notes="Organ: kidney; Vector: pME18s-FL3; Site_1: DraIII
(CACTGTGG); Site_2: DraIII (ACCACTGTG); 1st strand cDNA
was primed with an oligo(dT) primer
[ATGTGGCCCTTTTTTTTTTTTTT]; double-stranded cDNA was
ligated to a DraIII adaptor [TGTGGCCACTGTGG], digested
and cloned into distinct DraIII sites of the pME18s-FL3
vector (5' site CACTGTGG, 3' site CACTGTGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTTTCGCTTAAAGCTGG and 3' end
primer CGACCTGCAGCTCGACACA."

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BASE COUNT	208 a	154 c	180 g	235 t		
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Query Match		22.7%	Score 162.6;	DI 16;	Length 777;	
Best Local Similarity		54.3%	Pred. NO. 7.3e-35;			
Matches 378; Conservative			0; Mismatches 309;	Indels 10;	Gaps 2;	

	Query Match	22.7%	Score 162.6	DI 16	Length 777
	Best Local Similarity	54.2%	Prod. No. 7.3e-35		
	Matches 378	Conservative	0	Mismatches 309	Indels 10
	Gaps				
QY	29	tcttgctcctgcagactctctctgtgttgctgtggattctctgggaaagtcctggtgtggc	88		
Db	74	TCCGTCTCCAGCTGAGTGGCTCTTTTGGATCTGGACTGTGGAAAGTGCTGTGTGGC	133		
QY	89	cctgtgacatgagccattggcttaatgtcaaggtcattctagaagagctcatagtgaag	148		

[illegible]

267	QY	-----attgttgacctgagctctgaatgtcttgcaggcttatcaacctggtgcaaatcag	319
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320	QY	ttataaaatt-aaatgatttttttggtaaataagaggaaactttaaaaatgatgtgtgag	378
374	Db	TCTTAATGTCGAAGAAGAAATGGTTGGGTAGATCAAAATATTTTGAAGAGTCTCTGTAAA	433
379	QY	agctttatctacaatcagacacttatgaagaagctacagcaccaccaactcagatgttaacg	438
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[illegible]





Qy	589	acaggactaacagacagaatgacaccttctggaagagataaaaaatcaatgcctttcagtt	648
Qy	630	TCAGAACTAAGTGACCATGACATTTGCAGAAAGGGTCAGAAATATGTTGCAGGTG	689
Qy	649	tgttccactcttgattcaggattacgacatcatctttttggaagagtttttatagtaag	708
Db	690	CTTTTGTGACTTTTGGTTTCAACAATTAACGAGAAATCCTCGAATCAGTTTACAGTAT	749
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Db	750	gttctag 756	
RESULT	10		
LOCUS	AI530408		
DEFINITION	18-MAR-1999		
ACCESSION	AI530408	996 bp	EST
KEYWORDS	Mus musculus		
SOURCE	Mus musculus		
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus;		
REFERENCE	1 (bases 1 to 996)		
AUTHORS	Marra,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T., Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schuck,R., Ritter,E., Kohn,S., Shin,T., Jackson,J., Cardenas,M., McCann,R., Waterston,R. and Wilson R.		
TITLE	The WashU-NCI Mouse EST Project 1999		
JOURNAL	Unpublished (1999)		
COMMENT	Contact: Marra M/WashU-NCI Mouse EST Project 1999 Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@wustl.edu This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information.		
FEATURES	MGI:974219		
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BASE COUNT	273 a	180 c	223 g 316 t
ORIGIN	4 others		



[illegible]



[illegible]

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